

Amendments to the claims:

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a substantially purified Avilll peptide with cellulase activity and, said Avilll peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme having at least 70 90% identity to SEQ ID NO. 1, said Avilll peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, the catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (Avilll_Aac):

GH74_Ace ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWPPLLDWVG
 AvI!!_Aac AASQAYTWNKVA/TGGGGGFTPGIVFNPNSAKGVAYARTDIGGAYRRLNSDD-TATPLMDWVG

GH74_Aee WNNWGYNGVVSIAADPINTNKWAAGVGMYTNSWDPNDGAILRSSDQGATWQTPLPFKLG
AvIII_Aac NDTWHWDGIDALATDPVTDTRVYVAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPFKVG

GH74_Aee GNMPGRCGMGERLAVDPNNDNILYFGAPSGKGLWRSTDGATWSQMTNFPDVGTYIANPTD
AvIII_Aac GNMPGRCGMGERLAVDPNKNSLYFGARSQHGLWKSTDYCATWSNVTSTWTGTYFQDSSS

GH74_Ace TTGYQSQQVAAA/AFDKSSSLCQASKTIFVGVADPNPWFWSRDGGATWQAVPGAP-T
AvIII_Aac T YTSDPVGIAWVTFDSTSAGSSGSATPRIFVGVADACKSVFKSEDAGATWAWVSGEPQY

GH74_Aae — GFIHKGVFDPVNHLYIATSNTGGPYDGSSGDAVAKFSVTSGTWRISPVPTDTANDYF
 AvIII_Aac — CFLPHIKGVLSPEEKTLIYSYANGACPYDGNTGTVHKYNITSGVWTDISP-TSLASTYY

GH74_Ace GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIDWTSYPNRSRLRYVLDIS
AvI11_Aac CYCGGLSVDILOVPGTIVYAALNCWAWPDELLERSTDSCATWSPIEWNGYPSINYYYSYDIS

GH74_Aee AEPWLTFGVQPNNPPVSPKLGWMDEAMIAIDPFDNSDRMLYGTGATLYATNDLTWKWDGG
AeIII_Aee NAPWIDDTSTDOER VRVGCWMVFAALPDRDSNHLYVCTGLTVYGGHDITNWWDISKHNV

CH74_Acc_HIARMVKLFEETAVNDLSPRSGAPLISALCDLCCETHADVTAVRSTIETSPVETTGTGV

GH74_Aac HIAPMVKGLEETAVNDLSPPSGAPLISALCDEGGHIIADVIAVPSHTFSPVFTTGTGV
AvIII_Aac TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHPTYGTNTNGI

GH74_Ace DYAELNPSIIVRAGSFDPSSQPNDRHVAFTDGGKNWFQGSEPGVTTGGTVAAASADGSR
Avilll_Aac DYAGNKPNSIVRSGASDDYP TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT

GH74_Ace FVWAPGDPGQPVYAVCFGNSWAASQGVPAQIRSDRVNPKTFYALSNGTFYRSTDGGV
Avilll_Aac VLLMSSTSGALVSKSQG TLTAVSSLPSGAVIASDKSDNTVYGGSAGAIYVSKNTAT

GH74_Ace TFQPVAAGLPSSGAV/GVMFHAVPGKECDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
Avilll_Aac SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF

GH74_Ace GFGKSAPGSSYPAVFVGTICCGVTGAYRSDDCGTTAVLINDDQHQYGN-WGQAITGDHAN
Avilll_Aac GFGKASSTGSYVVIYGFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVNGDLQT

GH74_Ace LRRVYIGTNGRCIVYGDIGGAPSG
Avilll_Aac YGRVFRGHERPGHILLRQSQREPAG

2. (Previously Amended) The composition of claim 1 wherein the Avilll peptide is further defined as comprising a linker and a signal sequence.

3. (Previously Cancelled)

4. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the Avilll peptide is further defined as comprising a length of about 80 to about 150 amino acids.

5. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the Avilll peptide is further defined as comprising a length of about 90 amino acids.

6. (Previously Amended) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.

7. (Previously Amended) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.

8. (Previously Amended) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Previously Amended) The composition of claim 1 wherein said Avilll protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Previously Amended) The composition of claim 1, wherein the catalytic domain of GH74_Ace has at least 90% sequence identity with SEQ ID NO: 3.

11. (Previously Amended) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.

12. (Previously Amended) An isolated Avilll peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Previously Amended) An industrial mixture suitable for degrading cellulose, such mixture comprising the Avilll polypeptide of claim 1.

15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[]

16-27 (Cancelled)

28. (Previously Amended) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;

- c) a polypeptide sequence of SEQ ID NO: 5;
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Previously Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Amended) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)

47. (New) The composition of claim 1 wherein said catalytic domain

GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII_Aac):

GH74_Ace WNNWGYNGVVSIAADPINTNKVWAAGMVTNSWDPNDGAILRSSDQGATWQTPLPFKLG
AvI8I_Aac NDTWDHWGIDALATDPVTDTRVYAVGMVTNEWDPNVGSILRSTDQGDTWTETKLKFVGG

GH74_Ace TTGYQSDIQGVVVVAFDKSSSLGQASKTIFGVVADPNPVWSRDGGATWQAVPGAP-T
 AvIII_Aac T-YTSDPVGIAWTFDSTGSSGSATPRIFGVVADAGKSVFKSEDAGATWAWVSGEPQY
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GH74_Ace GFIPHKGVFDPVNHVLYIATSTGGPYDGSSGDUWKFVSGTWRISPVPSTDANDYF
AvIII_Aac GFLPKHGVLSPPEEKTLYIISYANGAGPYDGTNGTVHKYNITSGVWTDISP---TSLASTYY

GH74_Ace GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSRLRYVLDIS
AvI88_Aac GYGGSLVLDLQVPGTLMVAALNCWWPDELIFRSTDGGATWSPIEWNGYPSSINYYSYDIS

GH74_Ace HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV
AvIII_Aac TVKSLAVGIEEMLAVGLITPPGGPALLSAVGDDGGFYHSLDAAAPNQAYHTPTYGTTNGI

GH74_Ace DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGVTTGGTVAASADGSR
AvIII_Aac DYAGNKPSIVRSGASDDYP----TLAASSNFGSTWYADYAASTSTGTGAVALSADGDT

GH74_Ace FWWAPGDPGQPVVYAVGFGNSWAASQGPANAQIRSDRVNPKTFYALSNGTFYRSTDGG
AvIII_Aac VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT

GH74_Ace TFQPVAAGLPSSGAVGVMFHAVPGKEGLWLAASSGLYHSTNGGSSWSAI-TGVSSAVN
AvIII_Aac SFTKTTS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF

GH74_Ace GFGKSAPGSSYPAVFVVGIGVTGAYRSDDCGTTLVNLINDDQHQYGN-WGQAITGDHAN
Avilll_Aac GFGKASSTGSYVIVYGGFTIDGAAGLFKSEADTNWQVISDASHGFGSGSANVVNGDLQT

GH74_Ace LRRVYIGTNGRGRIVYGDIGGAPSG
Avilll_Aac YGRVFRGHERPGHLLRQSQREPAG

48. (New) The composition of claim 47 wherein said Avilll peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

49. (New) A composition comprising a substantially purified Avilll peptide having at least 99% identity to SEQ ID NO. 1, said Avilll peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.

50. (New) The composition of claim 49 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII_Aac):

GH74_Ace ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDINGMYRWDAANGRWIPLLDWVG
Avilll_Aac AASQAYTWKNVTGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG

GH74_Ace WNNWGYNGV/SIAADPINTNKWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG
Avilll_Aac NDTWHWDGIDALATDPVTDTRVYAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPFKVG

GH74_Ace GNMPGRGMGERLAVDPNNNDNLYFGAPSGKGLWRSTDGATWSQMTNFPDVGTIANPTD
Avilll_Aac GNMPGRGMGERLAVDPNKNISLYFGARSGHGLWKSTDYGATWSNVTSTWTGTYFQDSSS

GH74_Ace TTGYQSDIQGVVVVAFDKSSSSLGQASKTIFVGVADPNNPVWSRDGGATWQAVPGAP-T
Avilll_Aac T--YTSDPVGIAWTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY

GH74_Ace GFIPHKGVDPPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYF
Avilll_Aac GFLPHKGVLSPEEKTLYIISYANGAGPYDGTNGTVHKYNITSGWTDISP---TSLASTYY

GH74_Ace GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSRLRYVLDIS
Avilll_Aac GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDGATWSPIWEWNGYPSINYYYYSYDIS

GH74_Ace AEPWLTFGVQPNNPPVSPKPLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTWWDSSGGQI
Avilll_Aac NAPWIQDTTSTDQFP--VRVGWMVEALAIIDPFDSNHWLGYGTGLTVYGGHDLTNWDSKHNV

GH74_Ace HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTGV
Avilll_Aac TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI

GH74_Ace DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKWNWFQGSEPGVTTGGTVAASADGSR
Avilll_Aac DYAGNPKPSNIVRSGASDDYP----TLASSNFGSTWYADYAASTSTGTGAVALSADGDT

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GH74_Ace  FWWAPGDPGQPVVYAVGFGNSWAASQGV PAN AQRSDRVNPKTFY ALSNGT F YRSTDGGV
Avilll_Aac VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTV FYGGSAGAIYVSKNTAT

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51. (New) The composition of claim 50 wherein said Avilll peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

52. (New) A composition comprising a substantially purified Avill peptide having an amino acid sequence identical to SEQ ID NO. 1, said Avill peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74 Ace) enzyme and a carbohydrate binding domain (CBD) III.

53. (New) A composition comprising a substantially purified Avilll peptide, said Avilll peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain GH74_Ace having a sequence that is at least 90% identical to SEQ ID NO. 3.

54. (New) The composition of claim 51 wherein said catalytic domain GH74_Ace has a sequence identical to SEQ ID NO. 3.